

OIPe

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/023,617

DATE: 01/15/2002
 TIME: 18:02:44

Input Set : A:\10448-123001.TXT
 Output Set: N:\CRF3\01152002\J023617.raw

ENTERED

4 <110> APPLICANT: Bandaru, Rajasekhar
 5 Meyers, Rachel A.
 7 <120> TITLE OF INVENTION: 55562 AND 21617, NOVEL HUMAN PROTEINS
 8 AND METHODS OF USE THEREOF
 11 <130> FILE REFERENCE: 10448-123001
 13 <140> CURRENT APPLICATION NUMBER: US/10/023,617
 13 <141> CURRENT FILING DATE: 2001-12-18
 13 <150> PRIOR APPLICATION NUMBER: 60/256,249
 14 <151> PRIOR FILING DATE: 2000-12-18
 16 <150> PRIOR APPLICATION NUMBER: 60/256,405
 17 <151> PRIOR FILING DATE: 2000-12-18
 19 <160> NUMBER OF SEQ ID NOS: 10
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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 24 <211> LENGTH: 3624
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (339)...(1361)
 32 <400> SEQUENCE: 1

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34	acgggcgggc	ggctgccggc	aggaggcgcc	gagccgggtg	actgccgcgg	cgggcacagt	120	
35	ccggggccac	agcgccgagc	ccgggcggga	gtggccccgc	gcaggcaggg	agcggcgccg	180	
36	cgcactccaa	cccggcgggc	acctcggggg	cgggcgcggg	gcgcagcctt	ctcgtccccg	240	
37	cctctgtgac	aagcgccccg	gagccgggag	cccgattgcc	gggctcgggg	tgggcgcgga	300	
38	cgcaggcact	gggctcgtgc	ggggcccccg	gcgtcgcg	atg aac atc	gtg gtg gag	356	
39					Met Asn Ile Val Val Glu			
40				1	5			
42	ttc ttc	gtg gtc	act ttc	aaa gtg	ctc tgg	gcg ttc	gtg ctg gcc gcg	404
43	Phe Phe	Val Val	Thr Phe	Lys Val	Leu Trp	Ala Phe	Val Leu Ala Ala	
44		10		15		20		
46	gcg cgc	tgg ctg	gtg cgg	ccc aag	gag aag	agc gtg	gcg ggc cag gtg	452
47	Ala Arg	Trp Leu	Val Arg	Pro Lys	Glu Lys	Ser Val	Ala Gly Gln Val	
48		25		30		35		
50	tgc ctc	atc acc	ggc gcc	ggc agc	ggc ctg	ggc cgc	ctc ttc gcg ctg	500
51	Cys Leu	Ile Thr	Gly Ala	Gly Ser	Gly Leu	Gly Arg	Leu Phe Ala Leu	
52		40		45		50		
54	gag ttc	gcc cgg	cgt cgg	gcg ctg	ctg gtg	ctg tgg	gac atc aac acg	548
55	Glu Phe	Ala Arg	Arg Arg	Ala Leu	Leu Val	Leu Trp	Asp Ile Asn Thr	
56	55		60		65		70	
58	caa agc	aac gag	gag acg	gct ggc	atg gtg	cgc cac	atc tac cgc gac	596
59	Gln Ser	Asn Glu	Glu Thr	Ala Gly	Met Val	Arg His	Ile Tyr Arg Asp	
60		75		80		85		
62	ctg gag	gcg gcc	gac gcc	gct gcg	ctg caa	gct ggg	aat ggt gag gaa	644
63	Leu Glu	Ala Ala	Asp Ala	Ala Ala	Ala Leu	Gln Ala	Gly Asn Gly Glu Glu	
64		90		95		100		

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66	gaa att ctg ccc cac tgt aac ttg cag gtt ttt acc tac acc tgt gac	692
67	Glu Ile Leu Pro His Cys Asn Leu Gln Val Phe Thr Tyr Thr Cys Asp	
68	105 110 115	
70	gtg ggg aag agg gag aac gtc tac ctg acg gct gaa aga gtc cgc aag	740
71	Val Gly Lys Arg Glu Asn Val Tyr Leu Thr Ala Glu Arg Val Arg Lys	
72	120 125 130	
74	gag gtt ggc gaa gtc tca gtc ctg gtc aat aat gct ggt gtg gtc tct	788
75	Glu Val Gly Glu Val Ser Val Leu Val Asn Asn Ala Gly Val Val Ser	
76	135 140 145 150	
78	ggg cat cac ctt ctg gaa tgt cct gat gag ctc att gag aga acc atg	836
79	Gly His His Leu Leu Glu Cys Pro Asp Glu Leu Ile Glu Arg Thr Met	
80	155 160 165	
82	atg gtc aat tgc cat gca cac ttc tgg acc act aag gct ttt ctt cct	884
83	Met Val Asn Cys His Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro	
84	170 175 180	
86	acg atg ctg gag att aat cat ggt cat att gtg aca gtt gca agt tcc	932
87	Thr Met Leu Glu Ile Asn His Gly His Ile Val Thr Val Ala Ser Ser	
88	185 190 195	
90	ttg gga ttg ttc agt act gcc gga gtt gag gat tac tgt gcc agt aaa	980
91	Leu Gly Leu Phe Ser Thr Ala Gly Val Glu Asp Tyr Cys Ala Ser Lys	
92	200 205 210	
94	ttt gga gtt gtg ggt ttt cat gaa tcc ctg agc cat gaa cta aag gct	1028
95	Phe Gly Val Val Gly Phe His Glu Ser Leu Ser His Glu Leu Lys Ala	
96	215 220 225 230	
98	gct gaa aag gat gga att aaa aca acc ttg gtt tgc cct tat ctt gta	1076
99	Ala Glu Lys Asp Gly Ile Lys Thr Thr Leu Val Cys Pro Tyr Leu Val	
100	235 240 245	
102	gac act ggc atg ttc aga ggc tgc cga atc agg aaa gaa att gag cct	1124
103	Asp Thr Gly Met Phe Arg Gly Cys Arg Ile Arg Lys Glu Ile Glu Pro	
104	250 255 260	
106	ttt ctg cca cct ctg aag cct gat tac tgt gtg aag cag gcc atg aag	1172
107	Phe Leu Pro Pro Leu Lys Pro Asp Tyr Cys Val Lys Gln Ala Met Lys	
108	265 270 275	
110	gcc atc ctc act gac cag ccc atg atc tgc act ccc cgc ctc atg tac	1220
111	Ala Ile Leu Thr Asp Gln Pro Met Ile Cys Thr Pro Arg Leu Met Tyr	
112	280 285 290	
114	atc gtg acc ttc atg aag agc atc cta cca ttt gaa gca gtt gtg tgc	1268
115	Ile Val Thr Phe Met Lys Ser Ile Leu Pro Phe Glu Ala Val Val Cys	
116	295 300 305 310	
118	atg tat cgg ttc cta gga gcg gac aag tgt atg tac ccc ttt att gct	1316
119	Met Tyr Arg Phe Leu Gly Ala Asp Lys Cys Met Tyr Pro Phe Ile Ala	
120	315 320 325	
122	caa aga aag caa gcc aca aac aat aat gaa gca aaa aat gga atc	1361
123	Gln Arg Lys Gln Ala Thr Asn Asn Asn Glu Ala Lys Asn Gly Ile	
124	330 335 340	
126	taagaatctt tttgtatgga atattacttc tatcagaaga tgatcaagat gtttcagtcc	1421
127	agtgcacatc agcattgctg acattttatg gattctaaac ttgtgtttgtt tcttttttaa	1481
128	atcaactttt taaaaaata aagtgtaaat taaccgacta gagtacttgg aaaatgtgat	1541
129	cagtacaagt gaacttaggt tgttgccaac agggctcctt taggcagaac ccagaaacca	1601

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130 gtcaaatctg tagagaagca gtgtgacatc ttcaggttac cattattttt taatgagcag 1661
131 gaagtctaga aatgataact agactgtatg tttcatgtgt gtgatttttc agaattccca 1721
132 gagtttactc attcttggtt ttaaactcta gccagttgac atcttcgcaa tttcaaggac 1781
133 tgatagtgtc gtattttctc acgttttcta agtttccgtt ttgcaaggcc taggtgactt 1841
134 tttcatgggtg tttgtatggt tagctctttt gaaaaggaat tttgaaatct ccatcaactg 1901
135 aagtaaatga tgtctgagtg ttacagtwaa ggtgaccaag tctcttttct aaagtcacaa 1961
136 tgactaaagt attagttgaa tttttttttt tttttttgat ggagtctcgc tctgtcacca 2021
137 ggctggagtg cagtagcaca atcacggctc actgcaatct ctgcctcccr gtttcaagtg 2081
138 attctgctgt ctcagcctcc caagtagctg ggactacagg catgcgccac cagcccagc 2141
139 taatttttgt atttttagta gagacggggt ttcacatgt tggtcaggat ggtctccatc 2201
140 tcttgacatt gtgatccacc tgcctcggcc tcccaaagtg ctgggattac aggcagagc 2261
141 cactgcaccc agccttgaat ttttaatttt atctctgata tacttcatta agtgtctgga 2321
142 gacctaatta tcctaaaaga tcatacattt tctacctatg aattttgctg catacagaaa 2381
143 gtgccctttc ctcaggaagt tgctgtgttt catttctttg gatggactct tatctagaat 2441
144 acatagcagc tctgcaaaga aacagttttt aaaaatggga acttctacat tgaaaagtcc 2501
145 ccatttttgt gccaaactatg attagtgaga ggaagaaatc ttattctatg gcatatgtat 2561
146 ggaagggtgt aaagattctt ttgaaagggt tattcacatt gtagaacagc aaatgacatt 2621
147 tttacagtat ttttttgtaa agcaaatat tttgtgcctt gaatttggtt tatgtgtatt 2681
148 agtgaaacat tgtaaagggt aacttctacc tctgtatcta aatgtatacc atccacttgt 2741
149 aaatgactat aaactattat gtgattgctt ttttttttag aatgtcttgt ttaaatagtg 2801
150 gccaatgttt aaggctgtta aaataagcca acttttacta attggggagt tttataaatg 2861
151 actgattaaa tttaaagaat taacttacat gcaatttgtt gattattagt tatcagcagt 2921
152 gttgtaagga aaattattgt gttttttttt atgatcatta tcccacttta ggtaaagaaa 2981
153 aatattggaa tggaatagtg ttgggaaaca gacattaaca acctagggtg cctgcactca 3041
154 aatagccgat gttactgtcc ctagattaga gacttgatta agggcttggt tgtacaaaaa 3101
155 gtggggaaac aatgccatga cctgtgtttt agtttggtct caccacagat caaatctgca 3161
156 ctgtgtctac atataggaaa ggtcctgggt tgtgctaatt ttcccaatgc aggacttgag 3221
157 gaagagctct gttatatgtt tccatttctc tttatcaaag ataaccaaac cttatggccc 3281
158 ttataacaat ggaggcactg gctgcctctt aattttcaat catggacctt aagaagtact 3341
159 ctgaagggtc tcaacaatgc caggtgggga cagatatact cagagattat ccaggctctg 3401
160 ctcccagcga gcttgagta caccagaccc tcttagagaa atctgttata atttaacaac 3461
161 ccacttatcc acctaaaaac tgaggaaagt cgtctttaca tctaatttta ttcttgtgtg 3521
162 ttataactta aacctatttc tatttttgtt tgttattgcc cttataaggg tgtccatctc 3581
163 caagttcaat aaactaattc atttaaaaaa aaaaaaaaaa aaa 3624

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165 <210> SEQ ID NO: 2

166 <211> LENGTH: 341

167 <212> TYPE: PRT

168 <213> ORGANISM: Homo sapiens

170 <400> SEQUENCE: 2

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172 1 5 10 15
173 Ala Phe Val Leu Ala Ala Ala Arg Trp Leu Val Arg Pro Lys Glu Lys
174 20 25 30
175 Ser Val Ala Gly Gln Val Cys Leu Ile Thr Gly Ala Gly Ser Gly Leu
176 35 40 45
177 Gly Arg Leu Phe Ala Leu Glu Phe Ala Arg Arg Arg Ala Leu Leu Val
178 50 55 60
179 Leu Trp Asp Ile Asn Thr Gln Ser Asn Glu Glu Thr Ala Gly Met Val
180 65 70 75 80

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181 Arg His Ile Tyr Arg Asp Leu Glu Ala Ala Asp Ala Ala Ala Leu Gln
182                               85                               90                               95
183 Ala Gly Asn Gly Glu Glu Glu Ile Leu Pro His Cys Asn Leu Gln Val
184                               100                               105                               110
185 Phe Thr Tyr Thr Cys Asp Val Gly Lys Arg Glu Asn Val Tyr Leu Thr
186                               115                               120                               125
187 Ala Glu Arg Val Arg Lys Glu Val Gly Glu Val Ser Val Leu Val Asn
188                               130                               135                               140
189 Asn Ala Gly Val Val Ser Gly His His Leu Leu Glu Cys Pro Asp Glu
190 145                               150                               155                               160
191 Leu Ile Glu Arg Thr Met Met Val Asn Cys His Ala His Phe Trp Thr
192                               165                               170                               175
193 Thr Lys Ala Phe Leu Pro Thr Met Leu Glu Ile Asn His Gly His Ile
194                               180                               185                               190
195 Val Thr Val Ala Ser Ser Leu Gly Leu Phe Ser Thr Ala Gly Val Glu
196                               195                               200                               205
197 Asp Tyr Cys Ala Ser Lys Phe Gly Val Val Gly Phe His Glu Ser Leu
198 210                               215                               220
199 Ser His Glu Leu Lys Ala Ala Glu Lys Asp Gly Ile Lys Thr Thr Leu
200 225                               230                               235                               240
201 Val Cys Pro Tyr Leu Val Asp Thr Gly Met Phe Arg Gly Cys Arg Ile
202                               245                               250                               255
203 Arg Lys Glu Ile Glu Pro Phe Leu Pro Pro Leu Lys Pro Asp Tyr Cys
204                               260                               265                               270
205 Val Lys Gln Ala Met Lys Ala Ile Leu Thr Asp Gln Pro Met Ile Cys
206                               275                               280                               285
207 Thr Pro Arg Leu Met Tyr Ile Val Thr Phe Met Lys Ser Ile Leu Pro
208 290                               295                               300
209 Phe Glu Ala Val Val Cys Met Tyr Arg Phe Leu Gly Ala Asp Lys Cys
210 305                               310                               315                               320
211 Met Tyr Pro Phe Ile Ala Gln Arg Lys Gln Ala Thr Asn Asn Asn Glu
212                               325                               330                               335
213 Ala Lys Asn Gly Ile
214                               340

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216 <210> SEQ ID NO: 3

217 <211> LENGTH: 1026

218 <212> TYPE: DNA

219 <213> ORGANISM: Homo sapiens

221 <400> SEQUENCE: 3

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223 gccgcggcgc gctggctggt gcggcccaag gagaagagcg tggcgggcca ggtgtgcctc      120
224 atcaccggcg ccggcagcgg cctggggcgc ctcttcgcgc tggagttcgc ccggcgctcg      180
225 gcgctgctgg tgctgtggga catcaacacg caaagcaacg aggagacggc tggcatggtg      240
226 cgccacatct accgcgacct ggaggcggcc gacgcgcgtg cgctgcaagc tgggaatggt      300
227 gaggaagaaa ttctgccccca ctgtaacttg caggttttta cctacacctg tgacgtgggg      360
228 aagagggaga acgtctacct gacggctgaa agagtcgcga aggaggttgg cgaagtctca      420
229 gtcttggtca ataattgctg tgtggtctct gggcatcacc ttctggaatg tcctgatgag      480
230 ctcatgaga gaaccatgat ggtcaattgc catgcacact tctggaccac taaggctttt      540
231 cttcctacga tgctggagat taatcatggt catattgtga cagttgcaag ttccttggga      600

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232 ttgttcagta ctgccggagt tgaggattac tgtgccagta aatttggagt tgtggggttt 660
233 catgaatccc tgagccatga actaaaggct gctgaaaagg atggaattaa aacaaccttg 720
234 gtttgccttt atcttgtaga cactggcatg ttcagaggct gccgaatcag gaaagaaatt 780
235 gagccttttc tgccacctct gaagcctgat tactgtgtga agcaggccat gaaggccatc 840
236 ctactgacc agcccatgat ctgcactccc cgccctcatgt acatcgtgac cttcatgaag 900
237 agcatcctac catttgaagc agttgtgtgc atgtatcggg tcctaggagc ggacaagtgt 960
238 atgtaccctt ttattgctca aagaaagcaa gccacaaaca ataatgaagc aaaaaatgga 1020
239 atctaa 1026

241 <210> SEQ ID NO: 4
242 <211> LENGTH: 1327
243 <212> TYPE: DNA
244 <213> ORGANISM: Homo sapiens
246 <220> FEATURE:
247 <221> NAME/KEY: CDS
248 <222> LOCATION: (367)...(1188)
250 <400> SEQUENCE: 4

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253 cggatacacc ttgcgaagaa tgccgcactc tccgccactc attccccact caccggcacc 180
254 cgctaaacct tcagcctgaa attttccctcc gaaggaagca gagcagagga agaactacca 240
255 agtgctacac tcaaagcctg ccgtgcgagt gagcgcgacc tccaaactga ggcatttttg 300
256 ttccggcgaa atccctccca ctcaggaaag tccctagaaa gagagcgag gcgcctgggg 360
257 tatcac atg acc act tcc cgg aag cgc agc aga ccc gct caa ctt cat 408
258 Met Thr Thr Ser Arg Lys Arg Ser Arg Pro Ala Gln Leu His
259 1 5 10
261 cct ggg ttg agg cgg agg aga act tcc aga att atg gcg aag tcc ggg 456
262 Pro Gly Leu Arg Arg Arg Arg Thr Ser Arg Ile Met Ala Lys Ser Gly
263 15 20 25 30
265 ctg agg cag gac ccg cag agc aca gct gca gcc act gtg cta aag cgg 504
266 Leu Arg Gln Asp Pro Gln Ser Thr Ala Ala Ala Thr Val Leu Lys Arg
267 35 40 45
269 gca gta gaa cta gat tcg gag tcg cgg tat ccg cag gct ctg gtg tgt 552
270 Ala Val Glu Leu Asp Ser Glu Ser Arg Tyr Pro Gln Ala Leu Val Cys
271 50 55 60
273 tac caa gag ggg att gat ctg ctc ctg cag gtt ctg aaa ggt acc aaa 600
274 Tyr Gln Glu Gly Ile Asp Leu Leu Gln Val Leu Lys Gly Thr Lys
275 65 70 75
277 gat aat act aag aga tgt aat ctc aga gaa aaa att tcc aaa tac atg 648
278 Asp Asn Thr Lys Arg Cys Asn Leu Arg Glu Lys Ile Ser Lys Tyr Met
279 80 85 90
281 gac aga gcg gaa aac ata aag aag tac ttg gac caa gaa aaa gaa gat 696
282 Asp Arg Ala Glu Asn Ile Lys Lys Tyr Leu Asp Gln Glu Lys Glu Asp
283 95 100 105 110
285 gga aaa tat cac aag caa att aaa ata gaa gag aat gca aca ggt ttc 744
286 Gly Lys Tyr His Lys Gln Ile Lys Ile Glu Glu Asn Ala Thr Gly Phe
287 115 120 125
289 agt tat gag tca ctt ttt cgc gaa tac ctt aat gag aca gtt aca gaa 792
290 Ser Tyr Glu Ser Leu Phe Arg Glu Tyr Leu Asn Glu Thr Val Thr Glu
291 130 135 140

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VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date